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Award Number:
W81XWH-12-2-0050

TITLE:
Breast Cancer Translational Research Center of Excellence FY12-14

PRINCIPAL INVESTIGATOR:
Craig D. Shriver, M.D., FACS, COL MC USA

CONTRACTING ORGANIZATION:
The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc.

Bethesda, MD 20817

REPORT DATE:
November 2013

TYPE OF REPORT:
Final Report

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: (Check one)

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REPORT DOCUMENTATION PAGE

Form Approved
OMB No. 0704-0188

1. REPORT DATE *(DD-MM-YYYY)*	**2. REPORT TYPE**	**3. DATES COVERED** *(From - To)*
November 2013	Final Report	24 August 2012 – 23 August 2013

4. TITLE AND SUBTITLE

Breast Cancer Translational Research Center of Excellence FY12-14

5a. CONTRACT NUMBER

5b. GRANT NUMBER
W81XWH-12-2-0050

5c. PROGRAM ELEMENT NUMBER

6. AUTHOR(S)

Dr. Craig D. Shriver, MD FACS, COL, MC, USA – Principal Investigator
Ms. Lee Bronfman, RN, MA, CCRP – Administrative Director

5d. PROJECT NUMBER

5e. TASK NUMBER

5f. WORK UNIT NUMBER

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)

The Henry M. Jackson Foundation for the
Advancement of Military, Inc.
6720A Rockledge Drive Suite 100
Bethesda, Maryland 20817

8. PERFORMING ORGANIZATION REPORT NUMBER

Cost Center Number:
306231- 1.00 -63941

9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)

Commander, U.S. Army Medical Research and
Material Command, ATTN MCMR-ZC-I
504 Scott Street
Fort Detrick, MD 21702-5012

10. SPONSOR/MONITOR'S ACRONYM(S)

USAMRAA

11. SPONSOR/MONITOR'S REPORT NUMBER(S)

12. DISTRIBUTION / AVAILABILITY STATEMENT

Approved for public release; distribution unlimited.

13. SUPPLEMENTARY NOTES

14. ABSTRACT

The WRNMMC Clinical Breast Care Project/Winder Research Institute will help lead the way in the 21st century in the crusade against breast disorders. The project will utilize a multidisciplinary approach as the standard of care for treating breast diseases and breast cancer. This multidisciplinary model integrates prevention, screening, diagnosis, treatment and continuing care, but the project is further unique in the incorporation of advances in risk reduction, informatics, tissue banking and research. These efforts focus on decreasing the morbidity and mortality of breast cancer among American women.

15. SUBJECT TERMS

Tissue Banking, Biomedical Informatics, Focused Research, Translational Research, Genomics, Proteomics, Risk Reduction, Comprehensive Breast Care

16. SECURITY CLASSIFICATION OF: UU			**17. LIMITATION OF ABSTRACT:**	**18. NUMBER OF PAGES**	**19a. NAME OF RESPONSIBLE PERSON**
a. REPORT	**b. ABSTRACT**	**c. THIS PAGE**			Lee Bronfman,RN,MA,CCRP
UU	UU	UU	UU	35	**19b. TELEPHONE NUMBER** *(include area code)* *301-295-3890*

Standard Form 298 (Rev. 8-98)
Prescribed by ANSI Std. Z39.18

Table of Contents

Comprehensive Reproductive System Care Program—Clinical Breast Care Project (CRSCP-CBCP)
Annual Report

COL Craig D. Shriver, M.D.; Principal Investigator and Director

I. Introduction

Objective/Hypothesis: Utilize our unique biorepository of well characterized biospecimens from a broad subset of patients with breast cancer and other breast diseases to broaden our knowledge of the etiology and pathology of breast disease. Leverage the technological advances in genomic and proteomic research to further our understanding of breast cancer through discoveries in molecular biology, pathway analysis and systems biology that can be readily translated in to the clinic.

Specific Aims
This project is structured around three major themes: clinically relevant molecular profiles, evaluation of genetic risk and tumor biology. These themes inform research across the five BTRC pillars: (1) Breast Cancer Risk Reduction; (2) Biorepository; (3) Focused Research (Genomics, Proteomics); (4) Biomedical Informatics; and (5) Clinical Care.

Study Design: The project utilizes a multidisciplinary approach for researching breast diseases and breast cancer. This multidisciplinary model integrates prevention, screening, diagnosis, treatment and continuing care, but the project is further unique in the incorporation of advances in risk reduction, biomedical informatics, tissue banking and translational research. The project is based on a Discovery Science paradigm, leveraging high-throughput molecular biology technology and our unique clinically well-characterized tissue repository with advances in biomedical informatics leading to hypothesis-generating discoveries that are then tested in hypothesis-driven experiments.

Relevance: The BTRC is the continuation of the Clinical Breast Care Project (CBCP) that has been ongoing for more than10 years. Its uniqueness and relevance has been attested to by numerous world-class cancer experts, from the innumerable public and private presentations made by CBCP investigators over the years, as well as by the extensive publication record of CBCP researchers. CBCP has developed the world's largest biorepository of human breast tissues and biospecimens. CBCP has one of the few fully integrated genomic and proteomic molecular biology research programs in the nation devoted exclusively to research in breast diseases that is linked directly to the clinic and the patients (translational research).

Background
Breast cancer is the most common non skin-related malignancy among women in the western world. It accounts for one-third of all cancers diagnosed. Age is the single most important risk factor for the development of breast cancer, as incidence and mortality both increase with age. However, a significant number of breast cancers are diagnosed among young women. Each year, over 10,000 new breast cancer cases are detected in women under the age of 40. Over 90% of these occur among women aged 30-39 years and 8 women per 10,000 in this age group die from breast cancer every year. Breast cancer is the single leading cause of death in women aged 40-49 years. Despite the low absolute risk of breast cancer in women under 40 years of age, the incidence is increasing in this age group. The incidence in younger

women is probably underestimated based on the current understanding of the biology of breast cancer. Given the doubling time of most breast carcinomas a one centimeter breast cancer is estimated to have been *in situ* for a period of four to six years. Cancers identified in women age 40 to 45 originated at an age (> 40) when screening mammography would not have been recommended. Thus, given current screening recommendations, many breast cancers that develop in the fourth decade of life are not discovered by standard screening methods until the woman is older. The age-specific incidence for breast cancer among African American women is two times that of white women among those 30-39 years of age and the breast cancer mortality rate is nearly two times higher for African American women as compared to Caucasian women (12.8 versus 6.6 per 10.000 women, respectively). These differences have been attributed to significant ethnic and racial variations in the stage of disease at time of diagnosis, prevalence of adverse patient and tumor-related prognostic factors, and differences in provided cancer treatment. African American women are diagnosed with later stage disease and more aggressive tumors than white women accounting for the poorer overall survival among African American women with breast cancer. Reduction in ethnic and racial differences in breast cancer treatment outcome is a principal aim of modem day health care, and aggressive screening programs in young women aged 30-39 to detect disease at an early stage could assist in achieving this goal and improving cancer-related survival.

Hypothesis/Rationale/Purpose

The Walter Reed Nation Military Medical Center and Windber Research Institute have partnered in the Clinical Breast Care Project (CBCP) since its inception. This program has become a leader in the fight against breast disorders and cancer. Recognition of this leadership has prompted Congress to establish the CBCP as the Breast Cancer Translational Research Center of Excellence (BTRC), one of five centers so designated by Congress in 2008. The project utilizes a multidisciplinary bed-to- bench- to- bedside approach as the standard for treating and studying breast diseases and breast cancer. This multidisciplinary model integrates advances in risk reduction, prevention, screening, diagnosis, treatment and continuing care with cutting edge research incorporating advanced methods from biomedical informatics, tissue banking, high throughput biology and translational research. These efforts focus on decreasing the morbidity and mortality of breast cancer among American women.

The BTRC currently utilizes the facilities, resources and expertise of the Walter Reed National Military Medical Center (WRNMMC), the Windber Research Institute (WRI), the Windber Medical Center (WMC) and the Anne Arundel Medical Center (AAMC). The BTRC fosters a collaborative and collegial working relationship with its partners, other government agencies, academic institutions, commercial/industry leaders, and other non-profit organizations. The CBCP has a five pronged approach to the study and treatment of breast disease based on five interlocking pillars: ***(1) Breast Cancer Risk Reduction; (2) Biorepository; (3) Focused Research (including: Genomics, and Proteomics Research); (4) Biomedical Informatics; and (5) Clinical Care.***

The overall purpose of the BTRC is to provide a balanced environment between the two competing and yet complementary research paradigms of hypothesis-driven research and

hypothesis-generating research, in a translational research organization that unites clinical capabilities (patients, nurses, clinicians) with research capabilities (genomics, proteomics, immunohistochemistry and whole genome DNA sequencing) to analyze molecular and developmental pathways that are central to the diagnosis and treatment of breast disease. The critical foundations to this approach are provided by the tissue biorepository and biomedical informatics platforms.

We believe that there are three broad areas where the BTRC stands poised to make major contributions to breast cancer research and its translation into clinical practice. These areas include the identification of molecular profiles of disease with high clinical relevance, deepening our understanding of the genetic risk of breast disease and the enhancement of our understanding of breast tumor biology. These three themes are supported by the five pillars of the BTRC. There is no doubt that our understanding of the biology of Breast Cancer in all of its various forms and manifestations remains incomplete. We believe that our high-value repository of biospecimens, our strong biomedical informatics infrastructure and our research base with strong internal and external collaborations puts us in an excellent position to make contributions to the understanding of breast disease that will have impact on the quality of life for breast cancer patients and their families.

Clinically Relevant Molecular Profiling: This is cross-cutting theme with clinical, risk assessment and basic research components. The primary focus of this theme is to evaluate the utility of existing molecular profiles that have relevance to risk assessment, diagnosis, prognosis and therapy in a clinical setting and to discover new profiles that can be evaluated in the clinic. Projects within this theme have well defined translational goals. The development of comprehensive and highly informative molecular profiles will be a foundation for the development and delivery of personalized/individualized medicine. A variety of research modalities will be used to identify these profiles including immunohistochemistry, gene and protein expression analysis and genetic profiling including Next Generation DNA Sequencing. Two major new initiatives are outlined below one involving the development and testing of clinically relevant immunohistochemical profiles for disease stratification and therapeutic guidance and the other using complete genomics sequencing of tumor and matched normal DNA to develop clinically relevant profiles that could aid in disease diagnosis, prognosis and therapy selection.

Genetic Risk: The rapid developments of high throughput genotyping and genomic sequencing of individuals has reminded the research community of the power of family studies in the assessment of genetic risk. Evaluating family risk and translating that into individual risk is the primary goal of this theme. There is both clear clinical relevance and a strong basic research component to this theme. Understanding the underlying biology of observed racial disparities in disease prevalence, presentation and outcome will also be a major part of this effort. The interaction of the theme with the Risk Reduction pillar of the BTRC and the number of projects outlined below that deal with research into the basis of the observed racial disparities in breast cancer morbidity and mortality point out the relevance of this theme to the overall goals of the BTRC.

Tumor Biology: A unique combination of resources and expertise put the BTRC in a strong position to further our understanding of the basic biology of breast disease including breast cancer. Many of the projects outlined in the Focused Research pillar address basic problems associated with tumor heterogeneity. The tumor microenvironment and stromal interactions, metastasis and recurrence, as well as the role of cancer stem cells and tumor evolution affecting the efficacy of treatment are emphasized. We firmly believe that a robust understanding of breast tumor biology is a key to the successful translation of the research preformed at the BTRC to the clinic.

II. Body

Ultimate Goals:

- Decrease morbidity and mortality of breast cancer among American women. The BTRC building upon the five pillars of the CBCP will help lead the fight against breast disorders.
- Continue to develop a comprehensive breast care center/system with a multidisciplinary team approach that enables health care providers to work towards the common goal of reducing the morbidity and mortality caused by breast disease.
- Empower women afflicted with breast cancer and other breast disorders, with the decision-making tools and an environment that enhances their quality of life and meets psychosocial needs of the patients and their families.
- To continue support and grow a world-class biorepository of biospecimens that enable research into diseases of the breast.
- Develop research facilities that drive world-class high-throughput translational research.
- Develop an integrated computational and biomedical informatics infrastructure with an integrated data warehouse that forms the foundation for analysis of research findings leading to new and actionable knowledge related to diseases of the breast.
- Empower the clinical staff with a physician decision support system incorporating our evolving understanding of breast cancer and other breast diseases from research both within and outside the BTRC.

Pillar Specific Goals and Objectives:

1. Breast Cancer Risk Reduction:

Current research shows there area number of risk factors that may influence the development of breast cancer. Identifying people with these risk factors and implementing closer surveillance and risk reduction techniques may detect cancer earlier. Earlier detection of breast cancer leads to better prognosis and outcomes. Calculations of risk are based on computer models extensively validated as accurate in identifying women at high risk. Genetic counselors can help individuals and families make decisions regarding testing. For those who do test positive for the BRCA1 or BRCA2 gene,

surveillance (mammography and clinical breast exams) can help detect the disease at an early stage. A woman who tests positive can also consider taking the drug tamoxifen, which has been found to reduce the risk of developing breast cancer by almost 50 percent in women at high risk. Clinical trials are now under way to determine whether another drug, raloxifene, is also effective in preventing breast cancer. The objectives for the Risk Reduction Pillar are:

- Identify the population of patients at above average risk for the development of breast cancer.
- Decrease this identified population's rate of breast cancer development.
- Analyze potential cost differential in the prevention of breast cancer development.
- Incorporation of newly identified markers of breast cancer risk into the assessment of breast cancer risk.
- Identify patients from families that might harbor mutations in the BRCA1 or BRCA2 genes and offer testing to identify these mutations
- Identifying families with unexplained high frequencies of breast cancer as potential research subjects

Hereditary breast cancer is suspected when there is a strong family history of breast cancer: occurrences of the disease in at least three first or second-degree relatives (sisters, mothers, aunts). Currently the only tests available are DNA tests to determine whether an individual in such a high-risk family has a genetic mutation in the BRCA1 or BRCA2 genes.

When someone with a family history of breast cancer has been tested and found to have an altered BRCA1 or BRCA2 gene, the family is said to have a "known mutation." Positive test results only provide information about the risk of developing breast cancer. The test cannot tell a person whether or when cancer might develop. Many, but not all, women and some men who inherit an altered gene will develop breast cancer. Both men and women who inherit an altered gene, whether or not they develop cancer themselves, can pass the alteration on to their sons and daughters.

But even if the test is negative, the individual may still have a predisposition to hereditary breast cancer. Currently available techniques can't identify all cancer-predisposing mutations in the BRCA1 and BRCA2 genes. Or, an individual may have inherited a mutation caused by other genes. And, because most cases of breast cancer are not hereditary, individuals may develop breast cancer whether or not a genetic mutation is present.

Genetic counselors can help individuals and families make decisions regarding testing. For those who do test positive for the BRCA1 or BRCA2 gene, surveillance (mammography and clinical breast exams) can help detect the disease at an early stage. A woman who tests positive can also consider taking the drug tamoxifen, which has been found to reduce the risk of developing breast cancer by almost 50 percent in women at high risk. Clinical trials are now under way to determine whether another drug, raloxifene, is also effective in preventing breast cancer.

The field of oncology/surgical oncology is an ever- changing one with new developments in both diagnosis and treatment. We propose to collect data from all patients in the WRNMMC Breast Translational Research Center determined to be at an elevated risk for developing breast cancer in order to assess risk factors in this population for developing the disease and track outcomes of preventive and therapeutic interventions. Analysis of outcome will include comparison of various treatment modalities/regimens with regard to efficacy, risks for failure, complications, and overall morbidity/mortality/survival. The patient population of WRNMMC can provide a significant number of patients to compare/contrast our findings with those of our civilian counterparts, specifically the Joyce Murtha Breast Care Center and the Pat and Lesly Sajack Breast Center at Anne Arundel Medical Center in Annapolis, Maryland. The database will also allow us to analyze breast cancer risk data to provide scientific-based evidence that will guide the general surgeon and medical oncologist in optimal care of the patient at an elevated risk for developing breast cancer.

Plan:

The risk Reduction Clinic at WRNMMC and at Joyce Murtha Breast Care Center (JMBCC) is a multi-disciplinary program designed to identify, counsel and manage women at high risk for breast cancer. Patients receive an in-depth personal and family health history by a world renowned medical oncologist. At WRNMMC 283 patients were seen, 84 telephone consults were conducted and 7 patients were walk-ins. and at JMBCC in Windber, PA 103 patients were seen.

Current research shows there are risk factors that may influence the development of breast cancer. Identifying people with these risk factors and implementing closer surveillance and risk reduction techniques may detect cancer earlier. Earlier detection of breast cancer leads to better prognosis and outcomes. Calculations of risk are based on computer models extensively validated as accurate in identifying women at high risk.

If patients are referred for genetic testing, as per the American Society of Clinical Oncology, counseling involves the following eleven points:

- Information on the specific test being performed
- Implications of positive and negative results
- Options for estimation without genetic testing
- Risk of passing a mutation to a child
- Technical accuracy of the test
- Possibility that the test will not be informative
- Fees involved in testing
- Risk of psychological distress
- Risk of insurance or employer discrimination
- Confidentiality issues
- Options for medical surveillance and screening following testing

It has been observed that healthy female relatives of individuals with ovarian or breast cancer tend to exaggerate their risk of incurring either form of cancer and, thus, accurate risk assessment is essential to quality genetic counseling for breast cancer. Breast cancer genetic counseling serves the goal of helping women to analyze their own and their relatives' risk of developing breast cancer.

In BRCA screening, genetic counselors offer services in compiling family histories, personalizing epidemiology, and, more recently, conducting genetic testing to empower healthy women of families stricken by breast cancer to alter their lifestyles and healthcare to ensure avoidance or early detection of breast cancer. In addition, breast cancer victims and healthy members of a single family can enable accurate screening of female family members by obtaining a sequence of their BRCA genes. Detection of a familial BRCA mutation in individuals outside of the Ashkenazi Jewish population requires time-consuming genetic analysis of a large number of affected and unaffected family members in order to identify the specific BRCA mutation for a particular family.

In addition to a dedicated medical oncologist who sees patients who may be at high risk for breast cancer, this program employs a full time Genetics Clinical Nurse certified by the Genetic Nursing Credentialing Committee. She manages a population of patients identified as being at high-risk for breast cancer. She implements detailed family pedigree analyses and statistical tools such as the Gail model to evaluate patients in-depth for potential chemoprevention strategies and participation in genetic, preventive and surveillance research projects in conjunction with in-house medical oncologists and /or NCI researchers.
She provides initial genetic evaluation and pre-test counseling for patients referred for consideration of breast cancer genetic testing. She provides in-depth post test counseling and long term follow up in conjunction with appropriate physician specialists and genetic counselors.
Counseling for patients at high risk for breast cancer may include prophylactic mastectomy, oopherectomy, salpingectomy and Tamoxifin. Tamoxifen (Nolvadex®) is a drug that interferes with the activity of estrogen, and has been used for almost 10 years to reduce the risk of breast cancer in women who are at increased risk of developing breast cancer.

Testing positive or negative for a BRCA mutation is simply a risk assessment, not a certainty of experiencing or avoiding, respectively, breast cancer. Individuals with a BRCA mutation have an 80% risk of developing breast cancer by age 80. Therefore, 20% of BRCA mutation carriers never develop breast cancer. A first-degree relative of a carrier who tests negative for the mutation has the same breast cancer risk as women of the general population, namely 11%.

2. Biorepository:

Although there have been remarkable improvements in breast cancer diagnosis and management, most of the complex molecular mechanisms associated with the onset, progression and/or severity of breast cancer are still not well understood. As part of the Breast Translational Research Center (BTRC) we carry out molecular, biochemical and histological analysis of breast tissue and/or blood and blood components from breast cancer patients to provide insights into the molecular mechanisms that may be relevant in the development of breast cancer and breast diseases. To achieve this aim, a large supply and a wide variety of good quality tissue samples are needed. Unfortunately, good quality donor breast tissue is extremely scarce and when available is often not backed by a comprehensive medical history and/or is not a good representation of the target population or study area. The non-availability of a steady and consistent supply of good quality tissue limits the systematic analysis of tissues and negatively impacts the generation of biologically useful information in research laboratories and by extension negatively impacts new findings that benefit clinical practice. The objective of this project is therefore the acquisition and banking of breast tissue, lymph nodes, serum/plasma and other blood derivatives from informed and consenting donors.

- Collect and store a broad spectrum of biospecimens from every patient undergoing a breast biopsy and/or breast surgery at WRNMMC, WMC, AAMC, and our affiliated hospitals, which consent to participate in BTRC IRB-approved protocols.
- Collect and store biospecimens (blood) from women who are free of breast disease who consent to participate in BTRC IRB-approved protocols to act as controls.
- Utilize the power of this extensive biorepository as a major resource for breast disease research.
- Leverage the BTRC biorepository to maximize the utilization of the repository, with BTRC leadership approval, for the overall benefit of breast cancer patients and research, as able and appropriate.
- Participate in national/international projects that can benefit from resources of the BTRC biorepository.

  Figure BB-1 shows the cumulative patient accrual into the CBCP protocols since 2002. These patients, who have been recruited and consented into the CBCP protocols at WRAMC, WRNMMC, AAMC, JMBCC and other participating CBCP clinical intake sites are the foundations of the translational research that has occurred within the CBCP and which will continue in the BC-TRCOE. From these patients we have collected and stored in our biorepository over 54,349 biospecimens (**Figure BB-1**) donated by 6,247 fully consented subjects to our IRB approved tissue and blood protocols. (**Figure BB-2**)

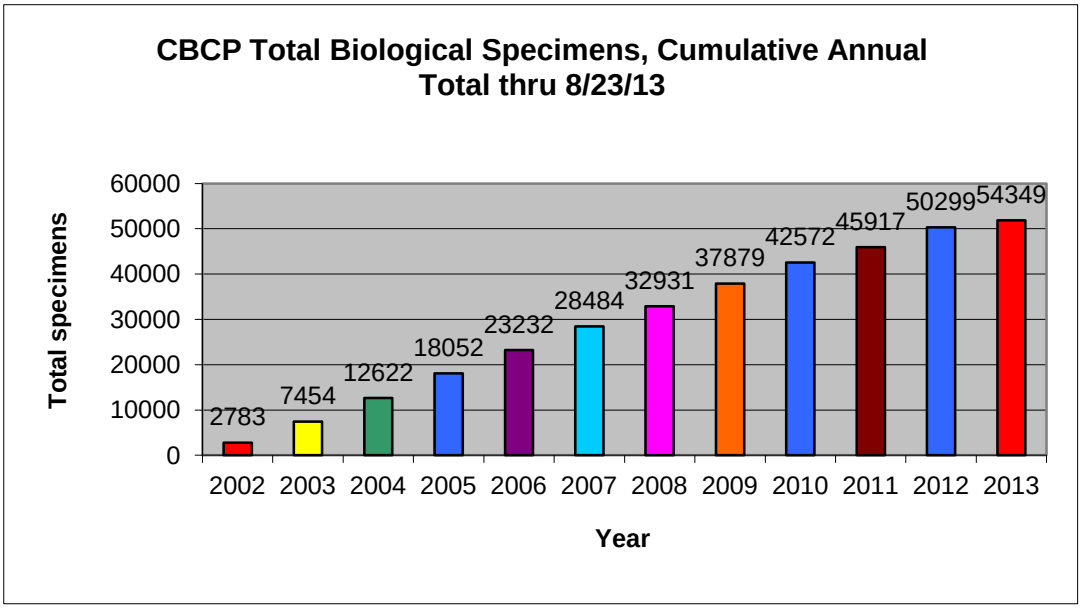


Figure BB-1. Total biospecimens collected and banked by the biorepository.

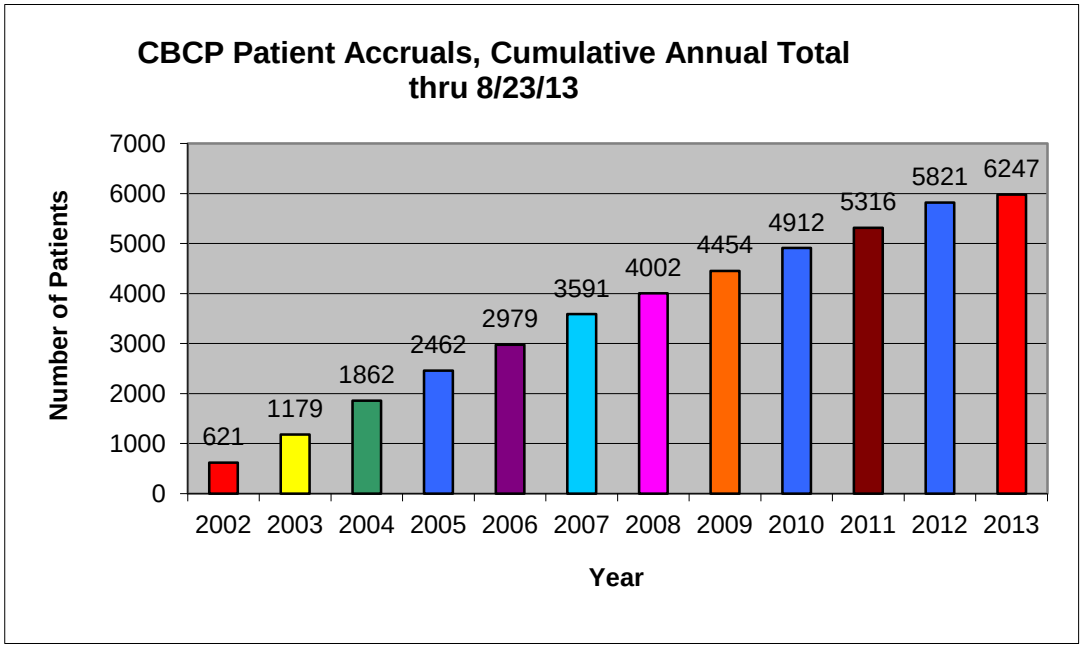


Figure BB-2 Cumulative patient accruals into CBCP protocols since 2002.

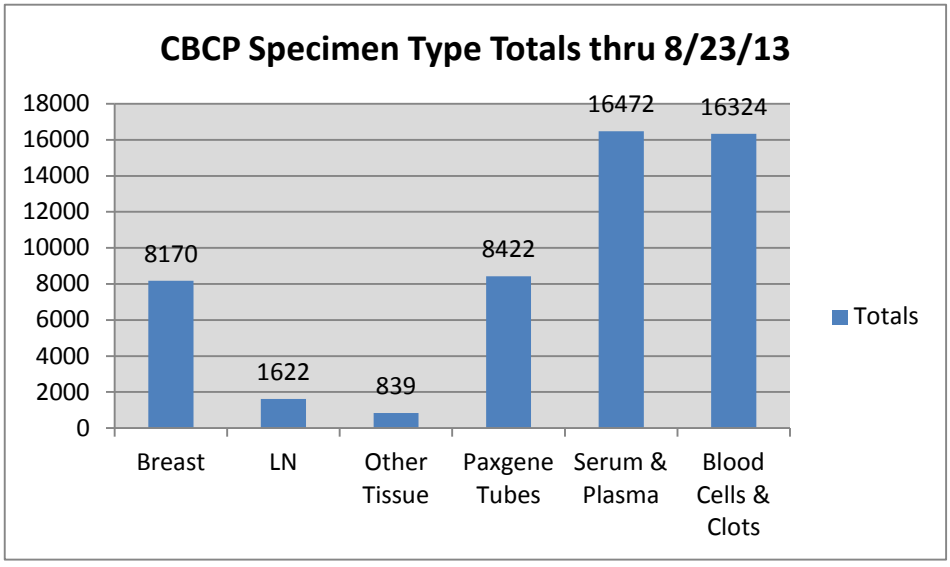


Figure BB-3. The numbers and types of biospecimens collected by the CBCP

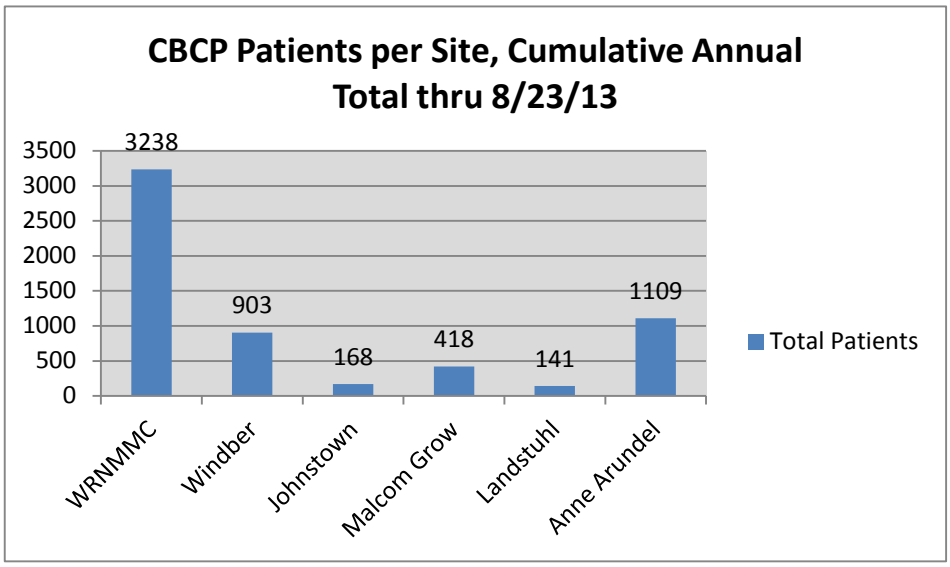


Figure BB-4. Numbers of patient recruited to CBCP protocols at various partner sites.

These specimens represent a broad spectrum of tissues, blood and blood products (**Figure BB-3**) that are not only a unique and valuable resource for the BC-TRC but are also the substrates for our translational research program. Along with the biospecimens that have been collected from CBCP participants, each consented patient also provides nearly 800 field of demographic, medical, life and family history data as well as complete pathology data on donated tissues. The collection of tissues that the BC-TRC inherits from the CBCP is even more valuable because of this rich annotation. Patients have been recruited from a number of partnering clinical intake sites over the history of the CBCP (**Figure BB-4**). At the start of the BC-TRC the active partners are WRAMC, the Joyce Murtha

Breast Care Center in Windber, PA, and the Anne Arundel Medical Center in Annapolis, MD.

3. Focused Research (including: Genomics and Proteomics Research):

The research pillar of the BTRC focuses on the translational research program involving the clinical programs at Walter Reed Army Medical Center's Breast Center and the Joyce Murtha Breast Care Center and the genomic and proteomic analysis carried out at the Windber Research Institute.

The following is a description of the projects that make up the Focused Research Pillar of the BTRC. This includes both ongoing and new projects. Major new initiatives include a major project that will generate complete genomic DNA sequence from breast cancer cases. Another new initiative will utilize immunohistochemical to generate clinically relevant profiles of breast tumors to better stratify the disease in terms of prognosis and treatment options.

Genomics: Utilize high-throughput and translational research in a unique Discovery Science environment to include but not be limited to:

- DNA analysis with genotyping studies, Copy Number Variation (CNV), gene sequencing and whole genome sequencing
- RNA/cDNA micro arrays, to identify expression level differentials across the entire spectrum of breast disease and from cancer specimens of all stages and types, as well as the accompanying lymph nodes and metastatic deposits, and blood.
- Measure epigenetic changes associated with disease
- Study molecular differences between breast tumors from African American and Caucasian women as the identification of such differences will allow for the development of more effective therapies that will improve outcomes in African American women with breast cancer.
- Perform whole genome DNA sequencing on DNA from 40 or more cases of breast cancer.
- Using state-or-the-art 3D cell culture techniques and modern approaches to the study of cancer cell biology, study the mechanisms of cell invasion, migration and ultimately metastasis in breast cancer cell lines.
- Use our unique collection of breast cancer biospecimens to characterize microRNA (miRNA) expression in breast cancer progression and metastasis.
- Identify genetic changes in low- and high-grade breast tumors to improve our understanding of the evolutionary process of breast cancer and to indentify a protein signature that can discriminate low- from high-grade breast tumors, allowing for more accurate diagnosis and risk assessment.
- Use our unique collection of breast cancer biospecimens to characterize molecular signatures that can differentiate primary breast tumors with and without metastatic potential, as well as between primary tumors and subsequent metastases.
- Improve our understanding of the molecular changes associated with HER2

amplification and over-expression to allow for more precise diagnosis of HER2+ patients and development of customized treatment options in patients with HER2+ breast cancer.

- Study the role of matrix metalloproteinases in breast cancer with the goal of developing diagnostic and prognostic marker of breast cancer based on expression of MMPs and polymorphisms in MMPs.
- Identify molecular alterations in the breast tumor microenvironment that contribute to tumorigenesis and which may lead to improved methods of breast cancer prevention and treatment.
- Use our unique collection of breast cancer biospecimens to study angiogenesis and lymphogenesis in different grades of DCIS and IDC.

Proteomics: Through collaboration with world class partners, utilize high-throughput and translational research in a unique Discovery Science environment to include but not be limited to:

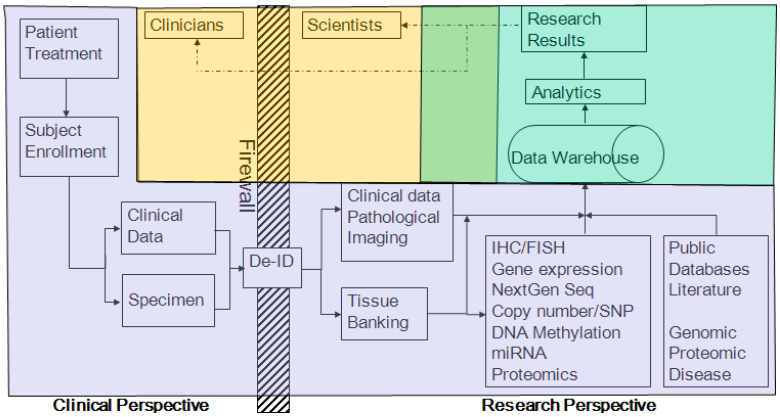
- Identify protein signatures associated with the development and progression of pre-malignant breast disease to improve our understanding of the biologic processes involved in early breast disease development and progression and to drive the development of personalized therapeutics for breast disease.
- Mass spectrometer pattern analysis and protein identification,
- Identify protein expression level differentials across the entire spectrum of breast disease and cancer specimens of all stages and types, as well as the accompanying lymph nodes and metastatic deposits, serum and blood
- Use Accurate Mass Tag (AMT) technology to assess protein expression changes in tumor tissues
- Search for novel protein biomarkers, individual or pattern.
- Store all this expression data in a data warehouse where it can then be utilized for biologic pathway development and in-silico biology research for hypothesis-driven research.

Collaborative Research: We have established a number of collaborations over the last several years that leverage the talents and resources of the BTRC to address research areas that would not have been possible using only our local resource base.

- Conduct quantitative analysis of therapy relevant proteins by immunohistochemistry within various subclasses of breast cancer to provide better patient selection into clinical trials for targeted and combination therapies.
- Perform affiliated translational laboratory research in support of the main expression profiling and biomarker discovery goals of the BTRC research laboratories.
- Develop alliances with other research organizations and entities and carry out project-supported research in support of same. Currently we have established collaborations with the Pacific Northwest National Laboratory, Vanderbilt University. The Institute for Systems Biology, the Thomas Jefferson University, the MGR Global, etc.

- Collaborate with the NCI/NHGRI TCGA (The Cancer Genome Atlas) project to study the genomics of breast cancer.

4. Biomedical Informatics:



Biomedical Informatics focuses on the management and utilization of biomedical information, and our view of its role in translational research is shown on the left figure. From the data flow point of view, it involves data collection and generation, where data tracking is needed (light blue). Cleaned data are then centralized in the data warehouse (light green), and subject to data analysis and mining for knowledge generation which is then presented to research scientists and clinicians to complete the two-way cycle of translational research (light yellow which partially overlaps with the data warehouse section).

As one of the original five pillars of the Clinical Breast Care Project, the Biomedical Informatics (BMIX) Group has become one of the foundations of the BTRC. The primary function of the BMIX team is the development and implementation of an infrastructure that supports the acquisition, storage, and maintenance of the clinical and molecular data generated by the Center. The successful accomplishment of this goal enables the development, implementation and support of the tools for data analysis that are necessary to achieve the research goals of the BTRC. The activities of this group requires that it both supports the research activities of the Center as well as carrying out research into new algorithms and methods that can lead to novel discoveries based on the unique resources, and data generated by this program. These functions are critical to meeting the translational research goals of the BTRC.

- Develop a comprehensive QA program and aid in SOP development for data collection and generation to ensure acquisition of high quality of data.
- Develop and support a robust laboratory information management system to ensure proper tracking of data acquisition.
- Develop and implement a clinically relevant and laboratory research-linked prospective, longitudinal computerized data warehouse to support translational research and ultimately support physician decision making
- Develop an analytical system including developing specific algorithms for integrative data analysis and mining, and deploying existing applications and algorithms to ensure execution of data analysis, mining, and modeling.
- Develop a breast knowledgebase to support clinical and research activities in BTRC..

- Develop other needed infrastructure to support the activities in all other BTRC pillars.
- Incorporate the rapidly growing public genomic and proteomic datasets related to breast cancer into our data warehouse to be able to mine the combined data sets for the generation of new hypotheses regarding breast cancer development, progression and treatment

5. Clinical Care:

This pillar of the BTRC is the foundation upon which all the success of our endeavors rests. Without patients enrolled in our biospecimen repository protocols, there would be no translational research center. These patients come from the clinical care environment. Since its inception in 2000, the CBCP (now the BTRC) has had as a priority, the development and staffing of the core clinical centers at Walter Reed National Military Medical Center, the Joyce Murtha Breast Care Center in Windber, PA and at our newest site, the Pat and Lesly Sajack Breast Center at Anne Arundel Medical Center in Annapolis, Maryland, that, under the direction of Lorraine Tafra, MD sees more than 500 newly diagnosed cases of breast cancer each year. The objectives of the Clinical Care Pillar are:

- Provide state of the art clinical care and treatment of patients seen in the Breast Translational Research Center at Walter Reed National Military Medical Center Bethesda.
- Decrease the negative psychological impact on the patient of having an evaluation or treatment intervention for breast disease by utilizing objective measurement instruments to longitudinally assess the patient's psychological response to evaluation and intervention, and base modifications of these procedures on those results.
- Create and maintain an environment (medical, physical, psychological) conductive to the multiple needs of the patient undergoing breast disease evaluation / treatment.
- Recruit patients into the various BTRC protocols to obtain the clinical data and biospecimens needed to meet the BTRC translational research goals.

This pillar of the BTRC is the foundation upon which the success of the former Clinical Breast Care Project and the current Breast Translational research Center rests. Without patients enrolled in our biospecimen repository protocols, there would be no translational research center. These patients come from the clinical care environment. Since its inception in 2000, the CBCP (now the BTRC) has had as a priority, the development and staffing of the core clinical centers at Walter Reed Army Medical Center, the Joyce Murtha Breast Care Center in Windber, PA and at our newest site, the Pat and Lesly Sajack Breast Center at Anne Arundel Medical Center in Annapolis, Maryland, that, under the direction of Lorraine Tafra, MD sees more than 500 newly diagnosed cases of breast cancer each year.

At each center the Staff is dually trained as clinical/research providers, to seamlessly integrate the need for a strong research focus in the clinical center with the requirement to provide state-of-the-art clinical care to the patients.

The care of our patients is provided by Physicians, Advance Practice Nurses (Nurse Practitioners) and Certified Breast Nurse Navigators with all personnel having the dual responsibility of clinical care and research. The Walter Reed National Military Medical Center, Joyce Murtha Breast Care Center and Pat and Lesly Sajack Breast Center at Anne Arundel Medical Center in Annapolis, Maryland, are state of the art facilities.

WRNMMC Breast Care Rehabilitation Clinical Research Program

Since 1999 the National Naval Medical Center (now Walter Reed National Military Medical Center) Breast Care department has utilized a Prospective Surveillance Model (PSM) of rehabilitation care for women with breast cancer. The PSM provides ongoing education and evaluation of women before, during and after breast cancer treatment. Interval assessment of function, strength, mobility and limb volume is an effective mechanism to identify impairments early and introduce treatment when the impairment is in a less severe state. This model has been studied in an ongoing clinical trial (NCT00513838) http://clinicaltrials.gov/ct2/show/NCT00513838 and demonstrates significant improvement in overall function and quality of life among breast cancer survivors.

The model is recognized as an emerging standard of care in both the national and international communities. http://www.washingtonpost.com/national/health-science/walter-reed-national-military-medical-center-tests-cancer-rehabilitation-model/2011/10/03/gIQAnu4daL_story.html

The PSM model will be featured in an upcoming supplement to the journal Cancer. A full supplement will be dedicated to highlighting the PSM and the evidence to support the model and it's components as a new standard of care in breast cancer.

The Multidisciplinary Conference

At the Walter Reed National Military Medical Center, we expect to see approximately 10,000 patients per year and will diagnose approximately 200 plus new breast cancers per year.

The Multidisciplinary Conference occurs every Thursday and the purpose of this day is to Provide an opportunity for the newly diagnosed breast cancer patient to meet all the providers that comprise the interdisciplinary breast care team. Providers include a breast surgeon, a medical oncologist, a radiation oncologist, a psychologist and /or social worker, nurse navigators/case managers, a physical therapist, and a plastic surgeon. Each specialty has individual private appointments to assess and evaluate each patient who, with significant others of their choice, is given a private room for the day. The benefit of the Multidisciplinary Conference Day is a one day visit to see all the various providers instead of having individual appointments spread over several days or weeks.
This allows us to educate, facilitate and coordinate a comprehensive breast treatment plan for the patient that maximizes treatment options and streamlines patient care in a patient-focused environment.

It also allows us to discuss the various research protocols with patients and, if they agree, obtain informed written consent and complete, with the assistance of a research nurse, an extensive questionnaire that captures more than 500 fields of clinical data.
The breast care team assembles and conducts an interdisciplinary conference to discuss each patient's case, resulting in a comprehensive treatment plan built on a team consensus. The results of the conference are then reviewed with the patient/family and time is provided to clarify and ask questions.

In an article entitled "*Hidden in Plain View – Integration of Effective Patient Partnerships with Evidence Based Medicine in the Military Health System –The Walter Reed Army Medical Center Clinical Breast Care Project"* the TEMPLATE day is described by the following quote "This method of physician communication and consensus avoids conflicting messages to the patient and allows for the best evidence-based approach. The literature supports the notion that a group decision is superior to sequential individual ones. Staff and patient satisfaction, stability of staff retention, and continuous improvement attitude, creates optimal outcomes in a safe, high quality, and supportive, attractive physical environment. As the Program Director NCC General Surgery Residency Director, clearly COL Shriver leads by example and has an impact on physicians during their graduate medical education by experiencing how idealized care can be operational zed in a military setting. This model of care should certainly be considered as the National Capital Area moves forward with the merger of Walter Reed Army Medical Center with the National Naval Medical Center and becomes the Walter Reed National Military Medical Center (WRNMMC) in 2011."

Military Relevance:

Breast cancer is the most common non-skin cancer in women. It is the single greatest cause of cancer deaths among women under 40, and is a significant cause of mortality for women in the United States Armed Forces. Breast cancer mortality among women <50 years of age accounts for >40% of years of life lost due to this disease. The economic, social and emotional costs to families are far greater when a young woman dies than when an older woman dies of breast cancer. The more aggressive nature of the disease in young patients along with the attendant costs underscores the importance of early detection of breast cancer in young women. Breast cancer is a curable disease if it is detected early; as such early detection is related to survivorship, cost of treatment and quality of life for the affected woman.

The majority (>90%) of women in active military service are < 40 years of age. The Department of Defense (DOD) with its high percentage of young women and its commitment to health care is particularly concerned about breast cancer. When discovered at a later stage, treatment of breast cancer is expensive, aggressive and results in considerable disruption to the woman's ability to contribute to society. Cost and disruption to life are considerably less when the carcinoma is discovered at an earlier stage. Furthermore, the DOD has a high percentage of African-American (~40%) and Hispanic (~10%) women. Death rates from breast cancer tend to be particularly high in these ethnic groups owing in part to later stage of detection and to the more aggressive

nature of breast cancer in these groups.

The active duty military force is approximately 20% female. Most of these service members are in the age range (30-40 years) where routine screening for breast cancer consists only of clinical breast examination. Both mammography and clinical breast examination have a very poor accuracy in the young active duty force in determining which breast abnormalities require treatment, and which are benign and can be left alone. The immense scale and impact of this problem for the military can be assessed by the fact that there were over 2,000 cases of breast cancer diagnosed in active duty service members over the last ten years (source: ACTURS DoD Tumor Registry data). Furthermore, there were over 8,000 unnecessary breast biopsies done on active duty women during this time because it takes 4 breast biopsies of normal non-cancerous lesions to find each individual breast cancer. Hence, women often need to take lengthy amounts of time off from duty in order to undergo multiple tests leading up to the biopsy as well as time off from duty because of the biopsy itself. This translates into approximately 10,000 weeks, or 30 person-years, of time lost in the evaluation of normal, benign breast lesions in active duty service members. This would be unacceptable for any other healthcare issue, and should be so for this one. Unfortunately, at the present time there is no screening tool available to diagnose breast cancer in the early, curable stages for women under the age of 40, who make up the vast majority of women in military uniform.

III. Key Research Accomplishments

Breast Cancer Translational Research Center of Excellence (BC-COE) Statement of Work

Task 1: Identify and counsel 100 patients annually at high risk for development of breast cancer, and employ risk reduction strategies. For the accomplishment, see page 9.

Task 2: Accrue over 500 patients annually to the "core" BC-COE protocols through consenting patients in the main BC-COE clinical sites. For the accomplishment, see pages 12, 13.

Task 3: Acquire through consented protocol acquisitions, over 5,000 specimens annually (neoplastic and non-neoplastic breast tissues and tumors, lymph nodes, metastatic deposits, blood and its components, bone marrow) on patients with all types of breast diseases and cancer. For the accomplishment, see page 12.

Task 4: Bank these biospecimens in the BC-COE Biorepository as the substrate for all molecular analyses carried out in BC-COE labs, as outlined in the BC-COE Core Protocols. Utilize this repository as the basis for intramural and extramural collaborations for secondary usage research. For the accomplishment, see page 12, 13.

Task 5: Perform focused research as outlined below on the biospecimens and clinical data collected under the BC-COE Core protocols including global expression analysis of

the DNA, RNA, and Protein features and including targeted research into genomic analysis of Stages I, II, and III breast cancer, DCIS, LCIS, and pre-malignant neoplasia. Present findings in peer-reviewed national meetings and publications.

Task 6: Perform whole genome DNA sequencing on DNA from 40 or more cases of breast cancer over the life of the project.
Data analysis on first samples has begun and we are selecting further samples for sequencing. Sequence analysis suggests that heterogeneous breast tumors have a common origin even though they are made up of multiple subtypes.

Task 7: Develop and support a robust laboratory information management system to ensure proper tracking of data acquisition and a clinically relevant and laboratory research-linked prospective, longitudinal computerized data warehouse to support translational research and ultimately support physician decision making.
The concept of LIMS is being re-assessed. Given the lack of a comprehensive system on the market that could satisfy our need, and given that research is dynamically evolving, we are putting together a 'data repository' concept that will not have a strong proceedural tracking capability but will have multiple data-input and dataloading interfaces which will be less cumbersome for the lab staff to use.

Task 8: Develop an analytical system for integrative data analysis and mining, and develop a breast knowledgebase to support clinical and research activities in BC-COE.
Subaim 1—we have compiled sample request forms and sample usage report for a list of samples and the projects the samples were used. Details are being worked out for the precise experimental platforms and result locations.
Subaim 2—in addition to gene expression microarrays form earlier projects that have been compiled earlier, we have now finished compiling the gene expression microarray data from other project for about 80 breast tissue samples, and are beginning to download and include RNASeq data from the TCGA project.
Subaim 3 and 4—no progress to report.

Task 9: Conduct quantitative analysis of therapy relevant proteins by immunohistochemistry within subclasses of breast cancer to provide better patient selection into clinical trials for targeted and combination therapies. - **ongoing**

Task 10: Study molecular differences between breast tumors from African American and Caucasian women as the identification of such differences will allow for the development of more effective therapies that will improve outcomes in African American women with breast cancer. **Completed, see abstract by Rummel, S., Penatzer, C., Sturtz, L., Shriver, C.,& Ellsworth, R.**

Task 11: Using state-or-the-art 3D cell culture techniques and modern approaches to the

study of cancer cell biology, study the mechanisms of cell invasion, migration and ultimately metastasis in breast cancer cell lines.

Aim 1.

CSPG4-NEDD9 interaction promotes triple-negative breast cancer progression and metastasis. We prepared several mutants of NEDD9 cDNA and currently generating transfectants in HCC38 cells for determining key domain(s) of NEDD9 to promote cell migration, invasion, and growth. We also constructed these mutants as recombinant proteins expressed in E.coli for identifying binding proteins and characterizing the mechanisms of migration, invasion, and growth. We are preparing a manuscript and will submit it in the next couple of months. As these studies progress, we are preparing a proposal the MCCFY13CSI cell line collaboration with Professor May Lou Cutler at USUHS. (see abstract by Iida, J., Dorchak, J., Clancy, R., Luo, C., Chen, Y., Hu, H., Mural, R., & Shriver, C.)

Aim 2.

Development of DNA aptamers against CD44 that inhibit breast cancer invasion and metastasis. We developed and characterized DNA aptamers against the exon v10 of CD44. The aptamers significantly inhibited migration and invasion of triple-negative breast cancer cells in vitro. We also demonstrated novel mechanisms of interaction of CD44 and EphA2 on cell surface. Since the aptamers that we developed markedly inhibited the binding of the exonV10 and EphA2, it is possible that the molecular complexes of CD44 and EphA2 play a key role in promoting triple-negative breast cancer invasion and metastasis. We submitted a grant NIH/NCI for further characterizing the mechanisms of CD44/EphA2 interaction and evaluate aptamers as potential therapeutic reagents. A manuscript describing this work is being submitted.

Aim 3.

Identification of drug-targets for triple-negative breast cancer. We developed systematic approaches to identify the targets by encompassing Biology, Bioinformatics, Animal models between WRI and USUHS. We are currently characterizing MIA and SOX10, which are highly expressed in triple-negative breast cancer tissues, for their biological functions in facilitating tumor growth, migration, and growth. This project is also receives some support from a USMCI-CCC grant in collaboration with Professor Mary Lou Cutler at USUHS.

Task 12: Use our unique collection of breast cancer biospecimens to characterize microRNA (miRNA) expression in breast cancer progression and metastasis. **Temporarily on hold.**

Task 13: Identify protein signatures associated with the development and progression of pre-malignant breast disease to improve our understanding of the biologic processes involved in early breast disease development and progression and to drive the development of personalized therapeutics for breast disease. **This task is ongoing.**

Task 14: Identify genetic changes in low- and high-grade breast tumors to improve our understanding of the evolutionary process of breast cancer and to indentify a protein signature that can discriminate low- from high-grade breast tumors, allowing for more accurate diagnosis and risk assessment.**Ongoing, awaiting further data analysis.**

Task 15: Use our unique collection of breast cancer biospecimens to characterize molecular signatures that can differentiate primary breast tumors with and without metastatic potential, as well as between primary tumors and subsequent metastases. **Ongoing, work will accelerate with new hire starting July 1, 2013.**

Task 16: Improve our understanding of the molecular changes associated with HER2 amplification and over-expression to allow for more precise diagnosis of HER2+ patients and development of customized treatment options in patients with HER2+ breast cancer.
Ongoing
Objective 1. Determination of the molecular status of genetically polysomic but clinically HER2 negative, tumors. When comparing the clinical characteristics of amplified versus polysomic patients, we found that amplified cases (N=44) were more likely to be ER negative (P=0.027) and have lymph node metastases (P=0.028) than polysomic cases (N=29). Although amplified cases tended to be younger at diagnosis and less likely to be diagnosed with Stage I tumors, this difference did not reach statistical significance. Tumor grade and size did not differ between polysomic and amplified samples. Polysomic (N=14) and amplified (N=18) cases were compared by gene expression microarray; 67 genes were identified as being differentially expressed (P<0.01; fold change >2) between the two groups. Thirty-nine genes were more highly expressed and 28 genes more lowly expressed in tumors with HER2 gene amplification when compared to tumors from patients with chromosome 17 polysomy. Genes with significant levels of differential expression between these two groups are involved in cell cycle control, cell adhesion and migration, cell differentiation, cytoskeleton organization, signal transduction, protein synthesis and degradation, and ion transport. Interestingly, the top 4 most significant genes with higher expression in the polysomic samples, including TUBG1, CPD, BLMH, and JUP, are all located on 17q. (see abstracts: Field, L., Deyarmin, B., Ellsworth, R., & Shriver, C and LA Sturtz, B Deyarmin, RE Ellsworth, CD Shriver.)

Objective 2. Determine how moderate expression of HER2 differs from no expression in patients with ER positive breast tumors
Completed (see abstract by Ellsworth, R., Valente, A., & Shriver, C.)

Task 17: Study the role of matrix metalloproteinases in breast cancer with the goal of developing diagnostic and prognostic marker of breast cancer based on expression of MMPs and polymorphisms in MMPs. **Complete. Publication 2012 in previous funding period.**

Task 18: Identify molecular alterations in the breast tumor microenvironment that contribute to tumorigenesis and which may lead to improved methods of breast cancer prevention and treatment. **(Complete)**

Objective 1. Gene expression profiling in lymph nodes harboring metastatic breast tumors to determine the role of the microenvironment in metastatic spread. Project completed. Manuscript describing results is in preparation. Poster describing results was presented at 2013 AACR meeting (abstract by Valente, A., Kane, J., Ellsworth, D., Shriver, C., & Ellsworth, R.). No further work needed

Task 19: Use our unique collection of breast cancer biospecimens to study angiogenesis and lymphogenesis in different grades of DCIS and IDC**. (This task is ongoing)**

Five types of tissues will be used: Normal, DCIS grade I, DCIS grade III, IDC grade I, IDC grade III. Each of them will contain 10 specimens. Antibodies for blood vessel-specific markers of CD31, CD 105 (endoglin), VEGFR1 and VEGFR2 will be used to measure MVD (micro-vessel density). Antibodies for lymphatic vesselspecific markers of podoplanin, alphaV integrin, beta3 integrin and VEGFR3 will be used to measure lymphatic MVD. Antibodies of breast cancer stem cell markers of CD44, CD24, and ESA will be used to detect the presence and the density of such cells. Data analysis will be multi-dimensional, based on MVD derived from each marker for each tissue.

1) The quality of each specimen and each marker will be assessed and extreme outliers will be excluded from further analysis.

2) Collective conclusions on blood vessel markers and lymphatic vessel markers on each of the 5 tissue types will be derived.

3) Relationships of angiogenic activities on the 5 tissue types will be derived.

4) Relationships of lymphangiogenic activities on the 5 tissue types will be derived.

5) Stem cell presence and density will be studied on the 5 tissues.

6) Relationships between angiognesis, lymphogenesis, and stem cells among the 5 tissues will be derived.

7) Relationships among the normal, low and high grade of DCIS and IDC will be derived based on angiogenic and lymphangiogenic activities as well as stem cell density.

8) Subtyping will be performed for all DCIS samples (ER, PR, HER2) (Zhou et al., 2009).

Task 20: Incorporate the rapidly growing public genomic and proteomic datasets related to breast cancer into our data warehouse to be able to mine the combined data sets for the generation of new hypotheses regarding breast cancer development, progression and treatment.

We have downloaded all the available TCGA clinical and molecular data. The molecular data includes, RNASeq, Exome DNA sequence, gene

expression microarray, DNA copy number from SNP microarray, DNA methylation, and reversed phase protein array.
Subaim 1. We have developed a preliminary inventory database for the sample-experiment relationship.
Subaim 2-5—no progress to report.
Instead of focusing on gene expression microarray data as originally planned, we believe that the RNASeq data contains more accurate information for gene expression and other information, and thus focused on processing the available RNASeq and clinical data, for over 800 patients. Using these data we have developed new research projects.

Key Research Accomplishments (continued)

- Further enhancements have been made to the database and data warehouse system that CBCP has developed for last five years, to integrate the clinical, molecular, pathologic, and biorepository aspects of CBCP translational research. The data warehouse and the On-Line Analytical Processing tool as the interface have proven to be a powerful tool in supporting scientific research at WRI and WRAMC and the underlying patient centric data model is being modified to support other types of disease.

- Gene expression difference have been found between African American women and Caucasian American women that may lead to insights into the differences in breast cancer severity seen between these populations. Recently we generated gene expression data from both tumors and non-malignant tissues from AAW and CW. 18 genes were differentially expressed in tumors and 13 genes in non-malignant breast specimens, including PSPHL, SOS1 and CRYBB2, which are differentially expressed in both tumors and non-malignant tissues.

- The Biomedical informatics core has continued development of the patient centric data model, enhanced tools for microarray data QA, and further analysis of breast disease co-occurrence.

- Numerous QA issues have been identified and entered into the QA Issue Tracking system for Walter Reed. At the same time a significant number of issues we previously reported have now been resolved by working with team at Walter Reed.

- We have published the results of an evaluation of Allelic Imbalance in non-neoplastic diseases, concluding that ADH and CCH are in fact, gnomically naive and that the multitude of studies that have evaluated pre-neoplastic lesions from breasts with invasive breast tumor cannot represent the status of pure early lesions.

- Copy number evaluation is being performed on fresh frozen genomic DNA samples from women with breast cancer, and a variety of pathological classifications using Affymetrix 500K SNP chips. Copy number and LOH analysis is being performed using Affymetrix genotyping console. Data have been presented in several different forums.

- In collaboration with Pacific Northwest Laboratory (PNNL) using the previously developed Accurate Mass Tag data base for proteins expressed in breast tissue we have examined breast tumors for the proteins that are markers of metastasis to lymph nodes.

- The current Clinical Laboratory Workflow System (CLWS) for tracking the information of clinical data and biospecimen collection and processing is gradually losing of the capability to support our needs and we have decided to develop a system to replace it.

- In this report period, we identified matched data elements in the MeSH, and the corresponded MeSH IDs have been extracted and put onto metadata files. Not all our data attributes are matched in MeSH. During this process, we discovered that some hierarchical structures in our data model could be rearranged. Such rearrangements have been implemented and the revised date model has been deployed in the Data Warehouse for Translational Research as of January, 2012.

- In this report period, we identified the needs to model new data elements (such as BRCA1/2, site, etc.). The workflows for loading the data for these elements have been developed and implemented. The next step is to incorporate these modules into the whole data model.

- The Data Correction Utility continues to serve its purpose, and 109 Core/Follow up and 19 Pathology Checklist corrections have been made in the DW4TR through the DCU.

- As an effort to continue developing the DW4TR, we started to drastically expand the sample-centric experimental modules to host other molecular data than what have already been covered, namely IHC, FISH, and gene expression microarray.

IV. **Reportable Outcomes**

23 August 2012 – 23 August 2013 Annual Report Numbers

Total Samples Collected:

Blood: 3647
Tissue: 1083
Lymph Node: 27

Other: 186

Total Patients Consented:

WRNMMC: 160
Windber: 96
AAMC: 303

CBCP Publications 23 AUG 2012 – 23 AUG 2013

Shriver CD. "A biomedical informatics infrastructure to support translational research" NCI Center for Biomedical Informatics & Information Tech Speaker Series, 5 Sep 2012

Greer LT, Rosman M, Mylander WC, Hooke J, Kovatich A, Sawyer K, Buras R, Shriver CD, Tafra L. "Does breast tumor heterogeneity necessitate further immunohistochemical staining on surgical specimens?" Association of Women Surgeons (AWS), September 2012, Chicago, IL, in conjunction with the American College of Surgeons 98th Annual Clinical Congress.

Iida J, Dorchak J, Lehman JR, Clancy R, Luo C, Chen Y, Somiari S, Ellsworth RE, Hu H, Mural RJ, Shriver CD. "FH535 inhibited migration and growth of breast cancer cells" PLOS ONE, 11 Sept 2012

Greer LT, Rosman M, Mylander W, Wareham J, Campbell JL, Hooke J, Kovatich A, Shriver CD, Tafra L. "Should immunohistochemical (IHC) markers be performed on axillary lymph node metastases in view of the lack of concordance between the primary tumor and axillary lymph node metastases?" American College of Surgeons 98th Annual Clinical Congress, 30 Sep-4 Oct 2012, Chicago, IL
]
Voeghtly LM, Mamula K, Campbell JL, Shriver CD, Ellsworth RE. "Molecular alterations associated with early and late breast cancer mortality" PLOS ONE, 4 Oct 2012

Shriver CD and Mural RJ. "Prestigious Journal to Publish Collaborative Breast Cancer Research" HJF newsletter 'SCOOP', Oct 2012

Ellsworth RE and Shriver CD. "Demographic differences in African American compared to Caucasian women with luminal A breast cancer" AACR, San Diego, CA, 27-30 Oct 2012

Rummel SE, Shriver CD, Ellsworth RE. " Evaluation of BRCA1 mutations in patients with family history of breast cancer" ASHG, 6-10 Nov 2012, San Francisco, CA

Valente AL, Rummel S, Shriver CD, Ellsworth RE "CDH1 mutations in patients with lobular carcinoma of the breast" ASHG, 6-10 Nov 2012, San Francisco, CA

Iida J, Dorchak J, Clancy R, Luo C, Chen Y, Hu H, Mural RJ, Shriver CD. "CSPG4-NEDD9 interaction promotes migration, invasion, and growth of breast cancer cells" ASCB, San Francisco, CA, 15-19 Dec 2012

Barrow TM, Barault L, Ellsworth RE, Harris HR, Valente AL, Shriver CD, Michels KB. "Aberrant methylation of imprinted genes is associated with triple-negative hormone receptor status in invasive breast cancer" Max Planck Freiburg Epigenetics Meeting, 5-8 Dec 2012, Freiburg, Germany

Valente AL, Kane JL, Ellsworth DL, Shriver CD, Ellsworth RE. "Molecular response of the axillary lymph node microenvironment to metastatic colonization" AACR, 4-8 Dec 2012, San Antonio, TX

Ellsworth RE, Valente AL, Shriver CD. "The effect of HER2 expression on luminal A breast tumors" SABCS, 4-8 Dec 2012, San Antonio, TX

Field L, Deyarmin B, van Laar R, Hooke J, Shriver C, Ellsworth R. "Molecular characteristics of breast tumor-associated adipose" SABCS, San Antonio, TX 4-8 Dec 2012

Kovatich AJ, Luo C, Chen Y, Hooke JA, Kvecher L, Rui H, Shriver CD, Mural RJ, Hu H. "Molecular subtypes of invasive breast cancers show differential expression of the proliferation marker Aurora Kinase A (AURKA)" SABCS, San Antonio, TX 4-8 Dec 2012

Chen Y, Bekhash A, Kovatich AJ, Hooke JA, Kvecher L, Mitchell EP, Rui H, Mural RJ, Shriver CD, Hu H. "Fibroadenomatoid changes are more prevalent in middle-aged women and have a positive association with invasive breast cancer" SABCS, San Antonio, TX 4-8 Dec 2012

Luo C, Iida J, Chen Y, Dorchak J, Kovatich AJ, Mural RJ, Hu H, Shriver CD. "Higher gene expression of CSPG4 in the basal-like subtype of invasive breast cancer and its negative association with lymph node metastasis" SABCS, San Antonio, TX 4-8 Dec 2012

Luo C, Chen Y, Kovatich AJ, Hooke JA, Kvecher L, Shriver CD, Mural RJ, Hu H. "p53 gene and protein expression patterns in human invasive breast cancers are correlated with its mutation status" SABCS, San Antonio, TX 4-8 Dec 2012

Dorchak J, Iida J, Clancy R, Luo C, Chen Y, Hu H, Mural RJ, Shriver CD. "FH535 inhibited migration and growth of breast cancer cells" SABCS, San Antonio, TX 4-8 Dec 2012

Luo C, Chen Y, Shriver CD, Hu H, Mural RJ. "Breast cancer subtype distribution among HapMap classified ethnic groups" SABCS, San Antonio, TX 4-8 Dec 2012

Rummel S, Varner E, Shriver CD, Ellsworth RE. "Evaluation of BRCA1 mutations in an unselected patient population with triple negative breast cancer" Breast Cancer Research and Treatment, Jan 2013

Barault L, Ellsworth RE, Harris HR, Valente AL, Shriver CD, Michels KB. "Leukocyte DNA as surrogate for the evaluation of imprinted loci methylation in mammary tissue DNA" PLOS ONE, 7 Feb 2013

Barror TM, Barault L, Ellsworth RE, Harris HR, Valente AL, Shriver CD, Michels KB. "Aberrant methylation of imprinted genes is associated with negative hormone receptor status in invasive breast cancer" Dana Farber Harvard Cancer Center, Breast and Gynecological Cancers symposium, 22 March 2013, Boston, MA

Rummel S, Penatzer C, Shriver CD, Ellsworth RE. "PSPHL and breast cancer in African American women: causative gene or population stratification?" AACR, Washington, DC, 6-10 April 2013

Barrow TM, Ellsworth RE, Harris H, Barault L, Velente A, Shriver CD, Michels KB. "Loss of imprinting in PEG3, MEST and ARHI/DIRAS3 in invasive breast cancer" AACR, 6-10 April 2013, Washington, DC

Greenspan R, O'Donnell A, Meyer J, Kane J, Mamula K, Deyarmin B, Larson C, Rigby S., Greenawalt A, Vatanian N, Mural R, Shriver C, Somiari S. "Tissue imprints and scrapings: assessing their potential as routine biobanking specimens for molecular research" Biopreservation and Biobanking Journal, submitted to publication in April 2013

Barrow, TM, Barault L, Ellsworth RE, Harris HR, Valente AL, Shriver CD, Michels KB. "Aberrant methylation of imprinted genes is associated with negative hormone receptor status in invasive breast cancer" Gordon Research Conferences: Cancer Genetics and Epigenetics, 21-26 April 2013, Lucca (Barga), Italy

Sato T, Tran TH, Peck AR, Girondo MA, Liu C, Goodman CR, Neilson LM, Freydin B, Chervoneva I, Hyslop T, Kovatich AJ, Hooke JA, Shriver CD, Fuchs SY, Rui H. "Prolactin suppresses a progestin-induced CK5-positive cell population in luminal breast cancer by a mechanism that involves inhibition of progestin-driven BCL6 expression" Oncogene Journal, 27 May 2013

Ellsworth RE, Penatzer C, Shriver CD. "Demographic and pathological differences between women treated in rural compared to urban-military breast cancer centers" ASCO, 31 May-4 June 2013

The Cancer Genome Atlas-Breast Cancer project team recently published a milestone research article in Nature (on-line Sep. 23, 2012; in print, Oct. 4, 2012, **CBCP Publications 23 AUG 2012 – 23 AUG 2013**

V. Conclusions

The breast Care center had its site visit by National Accreditation Program for Breast Centers (NAPBC) on August 9, 2012 resulting in full 3 year accreditation. The BTRC at Walter reed National Military Medical Center is the first NAPBC accredited Breast Care and Research Center in the DoD.

The WRNMMC-Bethesda hosted a Naming Ceremony for the WRNMMC Cancer Center on Dec 3, 2012, on the third floor of the America Building starting at 1300 hrs.

The Secretary of Defense was the keynote speaker durin this ceremony to officially name the Cancer Center after the late Congressman John P. Murtha; and to note the Cancer Center's recent achievement of being officially recognized by DoD as a Cancer Center of Excellence.

Richard Friedburg, the incoming president of CAP - College of American Pathologists, met with COL Shriver and select members of the Cancer Center on May 1, from 1400-1500 to learn more about the Murtha Cancer Center.

The John P. Murtha Cancer Center hosted its first Annual Cancer Awareness Day on Monday 24 June 2013 from 1000-1400 in the lobby of the America Building.

VI. Complimentary activities supported by separate funding

An article was published in the prestigious journal Nature (http://www.nature.com/nature/journal/v490/n7418/full/nature11412.html) entitled "Comprehensive molecular portraits of human breast tumors". The publication was accompanied with a press release from NIH and drew intensive attention from major news media.

Three components of the Clinical Breast Care Project, Walter Reed National Military Medical Center (WRNMMC), Windber Research Institute (WRI), and MDR Global, participated in this study. We functioned as a breast cancer tissue supplier, and we also participated in data analysis.

As a "Tissue Supplier" for the project, CBCP supplied over 10% of all the breast cancer cases used in the study. Among the 16 tissue suppliers, CBCP tissues were of the highest quality with a passing rate of 89.6%, and three batches passed at 100% which the director of the TCGA Program Office claimed as "amazing". CBCP tissues were procured following stringent Standard Operating Procedures and QA programs, and banked at the Tissue Banking facility at WRI following another stringent set of SOP and QA programs. The quality of CBCP tissues, is attested in this TCGA project.

The Biomedical Informatics group at WRI led the clinical data QA of the TCGA-BC project, and developed methods to examine and enhance the quality of data fields that are

important to the study. We also performed genomic data analysis. As part of the "Disease Working Group" for the project, we enforced the ASCO/CAP guidelines for HER2 clinical calls, and used additional molecular data to supplement such calls where needed. We authored Section II of the Supplementary Methods of the paper.

Work continues on a 6.7 million dollar Komen Promise grant awarded to Hallgier Rui of Thomas Jefferson University in 2009. On behalf of the Clinical Breast Care Project at Walter Reed Army Medical Center, the Henry M. Jackson Foundation is committed to participate as a consortium collaborator on this grant submission: **"Therapy-relevant Stratification of Breast Cancer Patients: Integrating Pathology and Biomarker Analyses"** As for the progress, Aim 1 of the grant involves the block and clinical data collection efforts and most of our work has been directed at this activity. The CBCP planned to submit approx. 500 cases. To date, we have collected blocks on 263 cases and have completed the clinical data forms on 196 cases. Of these 196 forms, we have performed a Quality Control check on 61 of them and sent them to the bioinformatics team for data entry testing. From the CBCP perspective, the next few months will also be directed at collecting blocks on the remaining 237 cases (approx.) and completing the completion and QC of all data forms.

All these three CBCP components are part of the Komen Promise Grant consortium. The CBCP authors in this paper are: Craig D. Shriver, Jeffrey A. Hooke, and Leigh Campbell from WRNMMC; Richard J. Mural, Hai Hu, Stella B. Somiari, Caroline Larson, Brenda Deyarmin, Leonid Kvecher, Yaqin Chen, and Chunqing Luo from WRI; and Albert J. Kovatich from MDR Global.

A protocol entitled:*An adaptive randomized Phase II Trial to determine pathologic complete response with the addition of carboplatin with and without veliparib to standard chemotherapy in the neoadjuvant treatment of triple-negative breast cancer* has been submitted to DRP (Department of Researech Programs)The study summary is below.

- **Study Summary**

Title	A Bayesian Adaptive randomized Phase II Trial to determine the impact on pathologic complete response with the addition of paclitaxel and carboplatin and paclitaxel, carboplatin, and veliparib to standard chemotherapy in the neoadjuvant treatment of triple-negative breast cancer.
Short Title	Neoadjuvant chemotherapy for triple-negative breast cancer
Protocol Number	Pending
Phase	Phase II

Methodology/Study Design	This is a randomized two-arm trial. The first 12 patients per arm (24 patients total) will be randomized in a standard fashion. Subsequent to this, based on Bayesian adaptation, according to pathologic complete response data, patients will have increased probability of assignment to arms according to response of patients enrolled to date. In this fashion, patients will be preferentially treated with more effective treatments.
Study Duration	It is estimated that it will take approximately 3 years to accrue and complete this protocol.
Study Center(s)	Thomas Jefferson University, Walter Reed National Military Medical Center, Anne Arundel Medical Center, and University of Pittsburgh Medical Center
Objectives	The primary objective of the study is to compare the pathologic complete response (pCR) in patients with Stage IIB, IIIA, IIIB, or IIIC triple negative breast cancer treated with paclitaxel and carboplatin or paclitaxel, carboplatin, and veliparib in addition to standard chemotherapy (adriamycin and cyclophosphamide). Secondary Objectives: • To determine relapse free survival • To determine overall clinical response to neoadjuvant therapy • To determine whether expression of 5 biomarkers (CK5, EGFR, ERCC1, Ki67, Parp1) correlate with a higher pCR in response to a particular treatment combination. • To determine whether tumors with biomarker signatures that are most like BRCA-mutated tumors (high expression of CK5 and high expression of EGFR), will correlate with a higher likelihood of pCR with treatment with a PARP inhibitor in combination with chemotherapy. • To determine whether tumors with high expression of the markers ERCC1, Ki67, and Parp1 will correlate with a higher rate of pCR with platinum agents in combination with paclitaxel or a PARP inhibitor. • To correlate levels of circulating tumor cells (CTCs) with pathologic CR. Exploratory Objectives: • To evaluate additional exploratory biomarkers based on evidence of possible prognostic or predictive value: CK14, CK17, Cyclin B1, CD44, CD24, Cyclin D1, Vimentin, Thymidine phosphorylase, ID4, p53, p63, p73, Dec1, phosphoHistoneH3, Thymidylate synthase, p16, gammaH2AX, Geminin, RAD51. • To determine which arms are best tolerated by patients with co-morbid conditions, such as hypertension and diabetes.
Number of Subjects	~80

Diagnosis and Main Inclusion Criteria	1. Histologically confirmed adenocarcinoma of the breast with the following markers: Estrogen receptor negative (<1%), progesterone receptor negative (<1%), and Her-2/neu negative (0, 1+ on IHC testing or 2+ and FISH ratio < 1.8). 2. Clinical stage IIB (T2N1, T3N0) or stage IIIA (T1N2, T2N2, T3N1, T3N2), IIIB, or IIIC breast cancer with no prior treatment for this tumor. 3. Complete radiology or tumor assessment within 28 days prior to enrollment. 4. ECOG Performance Status of 0 or 1.
Study Therapy, Dose, Route, Regimen	Veliparib (ABT-888) which will be given concurrently with paclitaxel and carboplatin in the study arm of this trial.
Duration of administration and follow-up	Intended duration of treatment is 24 weeks of neoadjuvant chemotherapy, followed by surgery within 12 weeks of completion of chemotherapy. Follow-up period is 3 years.
Statistical Methodology	This trial utilizes a Bayesian logistic regression model which assesses pCR of patients to date to increase the probability of assignment to arms demonstrating increased response.

VII. APPENDICIES

- ATTACHMENT 1 List of personnel receiving pay from the research effort from 24 August 2012 – 23 August 2013.

Current Staff, role and percent of effort on project:

Full Name	Role	Percent of Effort %
Basham,Janice B	Licensed Practical Nurse	42%
Boone,Jaime J.	Program Manager	37%
Bronfman,Eileen T	Administrative Director	43%
Chestang,Allan	Data Manager	43%
Eckhauser,Peggy Lee	Research Nurse	48%
Ellsworth,Rachel E.	Cancer Geneticist	49%
Hilton,Karrie R.	Assistant Head Nurse	46%
Kelley,Kay	Research Protocol Coord	38%
Kovatich,Albert	Scientist	14%
Means,Marilyn	Laboratory Assistant	43%
Miskovsky, Vicki	Admin Reviewer CCC Protocols	19%
Nielsen RN,Deborah A	Research Nurse	34%
Pangaro, Katherine	Clinical Oncology Resch Nurse	10%
Patterson,Carol M	Medical Assistant	47%
Smith,Stephanie R	Research Nurse	43%
Tracey,Dianne P.	Office Manager/Admin. Assist.	23%
Vilakazi,Patricia N.	Biomedical Informatics Coord.	49%
Wareham,Janet Andrea Yoder	Pathologists Assistant	48%
Williamson,Eric	Breast Center Administrator	46%
Yambaka,Baredu S.	Research Assistant	48%
Zhu,Kangmin	Assoc Dir for Epidemiology	11%
Zingmark,Rebecca N.	Histotechnologist	28%
Weiss, Raymond	Physician	22%
Cordes, Rosemarie	Research Nurse	13%

- ATTACHMENT 2 : Expenditures

Total Cumulative Expenditure
for award W81XWH-12-2-0050
August 2012 – August 2013

Personnel:	652,937.83
Consultants:	0.00
Supplies:	27,632.27
Equipment:	0.00
Travel:	18,910.05
Rent:	0.00
Other Direct Cost:	752,195.66
Sub award:	1,911,933.35
Total Direct Cost:	3,363,609.16
Indirect Cost:	218,153.46
Fee:	-
Total Program Cost:	**$ 3,581,762.62**